LLSSYO

260

261

TLRMTI

200

ALTMNI

201

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321

320 LLMHLG

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ALTERNATE_NAMES
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                                                                                                                                                                                                                                                                               192
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                                                                                                                                                                                                                                                   196
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              *binding_site carbohydrate (Asn) (covalent) *status
 #domain transmembrane #status predicted #label TM7\
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                WTPYNIVILLNTEQEF-FGLSNCESTSQLDQAFQVTETLGMTHCCINPIIYAFVGEKFRR
                                                                                                                                                                                                                                                                                            -GWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLF
                                                                                                                                                                                                                                                                                                                                    YSWRHFHTLRMTIFCLVLPLLVMAICYTGIIKTLLRCPS-KKKYKAIRLIFVIMAVFFIF
                                                                                                                                                                                                                                                 LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTRCQKEDSVYVCGPYFP--R-
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                                                                                                                           TTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINGKKLKCLTDIY
                                                                                                                                                                   TSYYD-DVGLLCEKADTRALMAOFVPPLYSLVFTFGLLGNVVVVMILIKYRRLRIMTNIY{\cal FM}3 1 {\cal TM}3 1
                                                         #checksum 1732
                                                                                                                                                                                                                                                                                                                                                                              Length 360;
                                                                                                                Indels
                                                                                                                                                        311 YLRHFFHRHLLMHLGRYIPFLPSEKLE-RTSSVSPSTAEPELS 352
                                             #disulfide_bonds #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                      YLSVFFRKHITKRFCKOCPVFYRETVDGVTSTNTPSTGEQEVS
                                                         #length 360 #molecular-weight 41063
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                                                                                                Pred. No. 5.17e-187;
                                                                                     Score 1438; DB 2;
                                                                                                                                                                                                                                                                    87; Mismatches
                                                                                                                                                          predicted
                                                                                         52.0%;
                                                                                                    53.4%;
                                                                                                                  Conservative EC1
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##residue ##Cross-r ##CIOSS-I #map_positic KEYWORDS #cross-refer ##molecul ##status #accession #authors #journal ACCESSIONS REFERENCE #title GENETICS #gene ORGANISM DATE

02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change

#formal_name Mus musculus #common_name house mouse

- monse

MIP-1 alpha receptor like-1

#type complete

I49340

ORGANISM

DATE

TITLE ENTRY